Site-specific recombination system to manipulate the plastid genome of higher plants

This application claims priority under 35 U.S.C. §119(e) to US Provisional Applications 60/155,007 and 60/211,139 filed September 21, 1999 and June 13, 2000 respectively, the entire disclosure of each of the above-identified applications is incorporated by reference herein.

FIELD OF THE INVENTION

This invention relates to the fields of transgenic plants and molecular biology. More specifically, DNA constructs and methods of use thereof are provided which facilitate the excision of target DNA sequences from transplastomic plants.

BACKGROUND OF THE INVENTION

Several publications are referenced in this application by author name and year of publication in parentheses in order to more fully describe the state of the art to which this invention pertains. Full citations for these reference can be found at the end of the specification. The disclosure of each of these publications is incorporated by reference herein.

The plastid genetic system of higher plants is highly polyploid. For example, in a tobacco leaf there are as many as 100 chloroplasts, each carrying ~100 identical genome copies, a total of 10,000 copies in a leaf cell. High-level protein expression, lack of pollen transmission and the feasibility to engineer polycistronic expression units make the plastid genome

an attractive alternative to nuclear engineering. Plastid transformation vectors often contain a selective marker, most commonly a spectinomycin resistance (*aadA*) gene, flanked by plastid DNA sequences targeting insertion of the marker gene by homologous recombination into the plastid gnome. Genes of commercial value but lacking a selectable phenotype are physically linked to the selective marker and the two genes are integrated together as a block of heterologous sequences. Plastid transformation is accomplished by biolistic DNA delivery or polyethylene glycol induced uptake of the transforming DNA followed by selection for the antibiotic resistance marker to ensure preferential propagation of plastids with transformed genome copies. As the result, all the 10,000 wild-type plastid genome copies in a cell are replaced with transgenic copies during a gradual process (Maliga, 1993).

Incorporation of a selectable marker gene is essential to ensure preferential maintenance of the transformed plastid genome copies. However, once transformation is accomplished, maintenance of the marker gene is undesirable. One problem may be the metabolic burden imposed by the expression of the selectable marker gene. For example FLARE-S, the product of the marker gene with good prospects to transform cereal chloroplasts, accumulates up to 18% of the total soluble cellular protein (Khan and Maliga 1999). The second problem is the relatively high potential for horizontal transfer of plastid marker genes to microbes (Tepfer 1989; Dröge et al. 1998; Sylvanen 1999), as commonly used plastid maker gene constructs are efficiently expressed in *E. coli* (Carrer et al. 1993; Svab and Maliga 1993). Therefore, having plastid marker genes in commercial products is undesirable.

SUMMARY OF THE INVENTION

In accordance with the present invention, methods and systems are provided which facilitate the manipulation of the plastid genomes of higher plants. The methods and systems of the invention may be employed to remove heterologous sequences from the plastid genome, such as selectable marker genes following successful isolation of transformed progeny. Alternatively, they may be designed to remove endogenous genes involved in plant cell metabolism, growth, development and fertility.

In one embodiment of the invention, a site specific recombination method for removal of predetermined nucleic acid sequences from the plastid genome is provided. The method comprises providing a first nucleic acid construct, the construct comprising a promoter being operably linked to a nucleic acid encoding an optional plastid targeting transit sequence which is in turn operably linked to a nucleic acid encoding a protein having excision activity, the construct further comprising a first selectable marker encoding nucleic acid having plant specific 5' and 3' regulatory nucleic acid sequences. The method also entails the use of a second DNA construct, the second construct comprising an second selectable marker encoding nucleic acid and excision sites. The second construct optionally contains a gene of interest and further comprises flanking plastid targeting nucleic acid sequences which facilitate homologous recombination into said plastid genome. The second DNA construct is introduced into plant cell and the cells are cultured in the presence of a selection agent, thereby selecting for those plant cells expressing the proteins encoded by said second DNA construct. The first DNA construct is

then introduced into cells having the second construct in the presence of a selection agent and those plant cells expressing proteins encoded by said first construct are selected. If present, the excising activity acts on the excision sites, thereby excising said predetermined target sequence. Plants may then be regenerated from plant cells obtained by the foregoing method.

Proteins having excision activity suitable for the practice of the invention include, without limitation, CRE, flippase, resolvase, FLP, SSV1-encoded integrase, and transposase. Sequences corresponding to excision sites suitable for the practice of the inventin, include, for example, LOX sequences, and *frt* sequences.

A variety of selection of agents may be selected. These include without limitation, kanamycin, gentamycin, spectinomycin, streptomycin and hygromycin, phosphinotricin, basta, glyphosate and bromoxynil.

In an alternative embodiment, a site specific recombination method for removal of predetermined nucleic acid sequences from the plastid genome is provided. The method comprising providing a first nucleic acid construct, said construct comprising a regulated promoter being operably linked to a nucleic acid encoding an optional plastid targeting transit sequence which is operably linked to a nucleic acid encoding a protein having excision activity, said construct optionally further comprising a first selectable marker encoding nucleic acid having plant specific 5' and 3' regulatory nucleic acid sequences. A second DNA construct is also provided, said second construct comprising an second selectable marker encoding nucleic acid and excision sites, said second construct further comprising flanking plastid targeting nucleic acid sequences which facilitate homologous

recombination into said plastid genome at a predetermined target sequence such that excision sites flank said predetermined target sequence following homologous recombination and introducing said second DNA construct into a plant cell. The plant cell so generated is then cultured in the presence of a selection agent, thereby selecting for those plant cells expressing the proteins encoded by said second DNA construct. A plant is then regenerated from cells containing the second construct and the first DNA construct is introduced into these cells in the presence of a selection agent and those plant cells expressing proteins encoded by said first construct are selected. The excising activity then acts on the excision sites, thereby excising said predetermined target sequence.

Regulatable promoters suitable for this embodiment of the invention include, without limitation, inducible promoters, tissue specific promoters, developmentally regulated promoters and chemically inducible promoters.

Candidate predetermined target sequences, may include for example genes associated with male sterility, clpP, ribosomal proteins, ribosomal operon sequences.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is a schematic diagram depicting CRE-mediated excision and integration of DNA segments.

Figure 2 is a map of a plastid transformation vector pSAC48, with *codA* bracketed by direct *loxP* sites. Positions of plastid genes *rrn16*, *trnV*, *rps12/7* (Shinozaki et al. 1986), the *aadA* and *codA* transgenes and relevant restriction sites are marked.

Figure 3 is a map of an *Agrobacterium* binary vector

pPZP212 with a plastid-targeted *Ssu-tp-cre* gene. Marked are: *Agrobacterium* Left and Right Border fragments; the kanamycin resistance (*neo*) gene; P2' promoter; SSU transit peptide (ssu-tp); *cre* coding region; recognition sequences for restriction enzymes *Bam*HI, *Eco*RI, *Hin*dIII, *Nco*I, *Nhe*I and *Xba*I.

Figure 4 shows maps of the plastid genome >*codA*> deletion derivatives. Shown are the plastid targeting region of vector pSAC48; the map of same region of the wild-type plastid genome (Nt-wt); the map of the plastid genome with CRE-mediated deletion of *codA via* the *lox* sites; and the map of the plastid genome with deletion via Prrn sequences lacking *trnV*, *aadA* and *codA*. Positions of plastid genes *rrn16*, *trnV* and *rps12/7* (Shinozaki et al. 1986), *aadA* and *codA* transgenes, primers (O1-O4) and relevant restriction sites (AI, *ApaI*; EV, *Eco*RV) are marked.

Figure 5 is a gel showing PCR amplification which confirms CRE-mediated deletion of *codA* from the plastid genome. Primers O1 and O2 (Fig. 3) amplified the 0.7-kb fragment of the deleted region. Same primers amplify the 2.0-kb *aadA-codA* fragment in tester lines Nt-pSAC48-21A and Nt-pSAC-16C (no transgenic Cre gene). No specific fragment was obtained in wild-type DNA sample and in Cre1-10 line. The lines obtained are listed in Table 1.

Figure 6 shows the results of DNA gel blot analysis wherein plastid genome structure was determined in the indicated plant samples. Total cellular DNA was isolated from the leaves of plants listed in Table 1 and digested with the *Apa*I and *Eco*RV restriction endonucleases. The probes were the wild-type *ApaI-EcoRV* plastid targeting

region and the *aadA* (*NcoI-XbaI* fragment) and *codA* (*NcoI-XbaI* fragment) coding regions. The hybridizing fragments are marked in Fig. 3.

Figure 7 are gels showing uniformity of plastid genome populations in the *Ssu-tp-cre* transformed plants. Total cellular DNA extracted from several leaves was probed with the *ApaI-EcoRV* targeting region probe. Numbers identify leaves from which DNA was extracted. For example, seven different leaves were probed from the Cre1-3 plant. For details, see Brief Description of Fig. 6.

Figures 8A and 8B are gels of PCR analysis confirming CRE-mediated deletion of *codA* in seedlings obtained by pollination with *Ssu-tp-cre* activator lines. 5-day old seedlings were tested from the cross Nt-pSAC48-21A as maternal parent and Cre2-200 and Cre2-300 activator lines as pollen parents. Amplification products are also shown for controls Nt-pSAC48-21A selfed seedling (48 self), wild-type (wt), the parental plant (48P) and the Cre1-3 plant. Fig. 8A: The *codA* region was amplified with the O1/O2 primers: the size of *aadA-codA* fragment is 2.0 kb; the *codA* deletion fragment is 0.7 kb (Fig. 4). Fig. 8B: Testing for *cre* sequences by PCR amplification with the Cre1/Cre3 oligonucleotides.

Figure 9 is a diagram of the plastid transformation pSAC38 with the >neo< bracketed by inverted lox sites. Positions of plastid genes rrn16, trnV and rps12/7 (Shinozaki et al., 1986), the aadA and codA transgenes and relevant restriction sites are marked.

Figure 10 shows a map of the plastid genome

containing the >neo< inversion construct. Shown are the plastid targeting region of vector pSAC38; the map of the same region of the wild-type plastid genome (Nt-wt); map of the plastid genome with CRE-mediated inversion of neo via the lox sites. Positions of the plastid genes rrn16, trnV and rps12/7 (Shinozaki et al., 1986) aadA and neo transgenes, primers (01-04) and relevant restriction sites (BamHI) are marked.

Figure 11 shows the results of DNA gel blot analysis for the determination of plastid genome structure of CRE-activated >neo< plants by DNA gel blot analysis. Total cellular DNA was digested with the BamHI restriction endonuclease. The probes was the wild-type *Apa*I-*Eco*RV plastid targeting region. The hybridizing fragments are marked in Fig. 10.

Figure 12 shows an exemplary monocistronic inversion vector. The gene of interest (*goi*) coding region is flanked by inverted *lox* sites (triangles). CRE activates *goi* expression by inversion, so that the coding strand is transcribed. *rrn16, trnV* and *rps12/7* are plastid genes (Shinozaki et al. 1986).

Figure 13 shows an alternative dicistronic *lox* inversion vector. Note that the inverted *lox* sites flank the selective marker (*aadA*) and *goi*, and only one gene is expressed. *rrn16, trnV* and *rps12/7* are plastid genes (Shinozaki et al. 1986).

Figure 14 shows a basic tobacco plastid *lox* deletion vector. The vector provides is a suitable backbone for vector construction and targets insertions into the *trnV-rps12/7* intergenic region.

Figure 15 shows a tobacco plastid *lox >aadA>* deletion vector. *rrn16, trnV* and *rps12/7* are plastid genes (Shinozaki et al. 1986).

Figure 16 shows a tobacco constitutive *>aadA>goi* dicistronic deletion vector. *rrn16, trnV* and *rps12/7* are plastid genes and are described in (Shinozaki et al. 1986).

Figure 17 shows a tobacco constitutive *goi >aadA>* dicistronic deletion vector. Note that vectors shown in Fig. 16 and Fig. 17 differ in the relative order of marker gene and the gene of interest. *rrn16, trnV* and *rps12/7* are plastid genes (Shinozaki et al. 1986).

Figure 18 shows a tobacco constitutive *goi >aadA>* dicistronic deletion vector, in which expression of *aadA* is dependent on translational coupling. Note that in this construct only one leader sequence is utilized. *rrn16, trnV* and *rps12/7* are plastid genes (Shinozaki et al. 1986).

Figure 19 shows a tobacco inducible *lox* deletion vector. Expression of *goi* is dependent on *aadA* excision. *rrn16, trnV* and *rps12/7* are plastid genes (Shinozaki et al. 1986). Abbreviations: P, promoter; T, 3' untranslated region; L1 is 5' leader sequence.

Figure 20 shows a vector suitable for Cre-mediated deletion of *clpP* gene from the plastid genome. The region of engineered plastid genome shown is the sequence contained in the plastid transformation vector. The *clpP* Exons are dark boxes, the Introns are open

boxes. Map position of plastid genes *psbB*, *rps12* Exon I and *rpl20* is also shown.

DETAILED DESCRIPTION OF THE INVENTION

The following definitions are provided to aid in understanding the subject matter regarded as the invention.

Heteroplastomic refers to the presence of a mixed population of different plastid genomes within a single plastid or in a population of plastids contained in plant cells or tissues.

Homoplastomic refers to a pure population of plastid genomes, either within a plastid or within a population contained in plant cells and tissues. Homoplastomic plastids, cells or tissues are genetically stable because they contain only one type of plastid genome. Hence, they remain homoplastomic even after the selection pressure has been removed, and selfed progeny are also homoplastomic. For purposes of the present invention, heteroplastomic populations of genomes that are functionally homoplastomic (i.e., contain only minor populations of wild-type DNA or transformed genomes with sequence variations) may be referred to herein as "functionally homoplastomic" or "substantially homoplastomic." These types of cells or tissues can be readily purified to a homoplastomic state by continued selection.

Plastome refers to the genome of a plastid.

Transplastome refers to a transformed plastid genome.

Transformation of plastids refers to the stable integration of transforming DNA into the plastid genome that is transmitted to the seed progeny of plants containing the transformed plastids.

Selectable marker gene refers to a gene that upon

expression confers a phenotype by which successfully transformed plastids or cells or tissues carrying the transformed plastid can be identified.

Transforming DNA refers to homologous DNA, or heterologous DNA flanked by homologous DNA , which when introduced into plastids becomes part of the plastid genome by homologous recombination.

Operably linked refers to two different regions or two separate genes spliced together in a construct such that both regions will function to promote gene expression and/or protein translation.

"Nucleic acid" or a "nucleic acid molecule" as used herein refers to any DNA or RNA molecule, either single or double stranded and, if single stranded, the molecule of its complementary sequence in either linear or circular form. In discussing nucleic acid molecules, a sequence or structure of a particular nucleic acid molecule may be described herein according to the normal convention of providing the sequence in the 5' to 3' direction. With reference to nucleic acids of the invention, the term "isolated nucleic acid" is sometimes used. This term, when applied to DNA, refers to a DNA molecule that is separated from sequences with which it is immediately contiguous in the naturally occurring genome of the organism in which it originated. For example, an "isolated nucleic acid" may comprise a DNA molecule inserted into a vector, such as a plasmid or virus vector, or integrated into the genomic DNA of a prokaryotic or eukaryotic cell or host organism.

When applied to RNA, the term "isolated nucleic acid" refers primarily to an RNA molecule encoded by an isolated DNA molecule as defined above. Alternatively, the term may refer to an RNA molecule that has been sufficiently separated from other nucleic acids with which it would be associated in its natural state (i.e.,

in cells or tissues). An isolated nucleic acid (either DNA or RNA) may further represent a molecule produced directly by biological or synthetic means and separated from other components present during its production.

The terms "percent similarity", "percent identity" and "percent homology" when referring to a particular sequence are used as set forth in the University of Wisconsin GCG software program.

The term "functional" as used herein implies that the nucleic or amino acid sequence is functional for the recited assay or purpose.

The phrase "consisting essentially of" when referring to a particular nucleotide or amino acid means a sequence having the properties of a given SEQ ID No:. For example, when used in reference to an amino acid sequence, the phrase includes the sequence per se and molecular modifications that would not affect the basic and novel characteristics of the sequence.

A "replicon" is any genetic element, for example, a plasmid, cosmid, bacmid, phage or virus, that is capable of replication largely under its own control. A replicon may be either RNA or DNA and may be single or double stranded.

A "vector" is a replicon, such as a plasmid, cosmid, bacmid, phage or virus, to which another genetic sequence or element (either DNA or RNA) may be attached so as to bring about the replication of the attached sequence or element.

An "expression operon" refers to a nucleic acid segment that may possess transcriptional and translational control sequences, such as promoters, enhancers, translational start signals (e.g., ATG or AUG codons), polyadenylation signals, terminators, and the like, and which facilitate the expression of a polypeptide coding sequence in a host cell or organism.

The term "oligonucleotide," as used herein refers to primers and probes of the present invention, and is defined as a nucleic acid molecule comprised of two or more ribo- or deoxyribonucleotides, preferably more than three. The exact size of the oligonucleotide will depend on various factors and on the particular application and use of the oligonucleotide.

The term "probe" as used herein refers to an oligonucleotide, polynucleotide or nucleic acid, either RNA or DNA, whether occurring naturally as in a purified restriction enzyme digest or produced synthetically, which is capable of annealing with or specifically hybridizing to a nucleic acid with sequences complementary to the probe. A probe may be either single-stranded or double-stranded. The exact length of the probe will depend upon many factors, including temperature, source of probe and use of the method. For example, for diagnostic applications, depending on the complexity of the target sequence, the oligonucleotide probe typically contains 15-25 or more nucleotides, although it may contain fewer nucleotides. The probes herein are selected to be "substantially" complementary to different strands of a particular target nucleic acid sequence. This means that the probes must be sufficiently complementary so as to be able to "specifically hybridize" or anneal with their respective target strands under a set of pre-determined conditions. Therefore, the probe sequence need not reflect the exact complementary sequence of the target. For example, a non-complementary nucleotide fragment may be attached to the 5' or 3' end of the probe, with the remainder of the probe sequence being complementary to the target strand. Alternatively, non-complementary bases or longer sequences can be interspersed into the probe, provided that the probe sequence has sufficient complementarity

with the sequence of the target nucleic acid to anneal therewith specfically.

The term "primer" as used herein refers to an oligonucleotide, either RNA or DNA, either single-stranded or double-stranded, either derived from a biological system, generated by restriction enzyme digestion, or produced synthetically which, when placed in the proper environment, is able to functionally act as an initiator of template-dependent nucleic acid synthesis. When presented with an appropriate nucleic acid template, suitable nucleoside triphosphate precursors of nucleic acids, a polymerase enzyme, suitable cofactors and conditions such as a suitable temperature and pH, the primer may be extended at its 3' terminus by the addition of nucleotides by the action of a polymerase or similar activity to yield an primer extension product. The primer may vary in length depending on the particular conditions and requirement of the application. For example, in diagnostic applications, the oligonucleotide primer is typically 15-25 or more nucleotides in length. The primer must be of sufficient complementarity to the desired template to prime the synthesis of the desired extension product, that is, to be able anneal with the desired template strand in a manner sufficient to provide the 3' hydroxyl moiety of the primer in appropriate juxtaposition for use in the initiation of synthesis by a polymerase or similar enzyme. It is not required that the primer sequence represent an exact complement of the desired template. For example, a non-complementary nucleotide sequence may be attached to the 5' end of an otherwise complementary primer. Alternatively, non-complementary bases may be interspersed within the oligonucleotide primer sequence, provided that the primer sequence has sufficient complementarity with the sequence of the

desired template strand to functionally provide a template-primer complex for the synthesis of the extension product. Amino acid residues described herein are preferred to be in the "L" isomeric form. However, residues in the "D" isomeric form may be substituted for any L-amino acid residue, provided the desired properties of the polypeptide are retained.

All amino-acid residue sequences represented herein conform to the conventional left-to-right amino-terminus to carboxy-terminus orientation.

The term "tag," "tag sequence" or "protein tag" refers to a chemical moiety, either a nucleotide, oligonucleotide, polynucleotide or an amino acid, peptide or protein or other chemical, that when added to another sequence, provides additional utility or confers useful properties, particularly in the detection or isolation, to that sequence. Thus, for example, a homopolymer nucleic acid sequence or a nucleic acid sequence complementary to a capture oligonucleotide may be added to a primer or probe sequence to facilitate the subsequent isolation of an extension product or hybridized product. In the case of protein tags, histidine residues (e.g., 4 to 8 consecutive histidine residues) may be added to either the amino- or carboxy-terminus of a protein to facilitate protein isolation by chelating metal chromatography. Alternatively, amino acid sequences, peptides, proteins or fusion partners representing epitopes or binding determinants reactive with specific antibody molecules or other molecules (e.g., flag epitope, c-myc epitope, transmembrane epitope of the influenza A virus hemaglutinin protein, protein A, cellulose binding domain, calmodulin binding protein, maltose binding protein, chitin binding domain, glutathione S-transferase, and the like) may be added to proteins to

facilitate protein isolation by procedures such as affinity or immunoaffinity chromatography. Chemical tag moieties include such molecules as biotin, which may be added to either nucleic acids or proteins and facilitates isolation or detection by interaction with avidin reagents, and the like. Numerous other tag moieties are known to, and can be envisioned by, the trained artisan, and are contemplated to be within the scope of this definition.

As used herein, the terms "reporter," "reporter system", "reporter gene," or "reporter gene product" shall mean an operative genetic system in which a nucleic acid comprises a gene that encodes a product that when expressed produces a reporter signal that is a readily measurable, e.g., by biological assay, immunoassay, radioimmunoassay, or by colorimetric, fluorogenic, chemiluminescent or other methods. The nucleic acid may be either RNA or DNA, linear or circular, single or double stranded, antisense or sense polarity, and is operatively linked to the necessary control elements for the expression of the reporter gene product. The required control elements will vary according to the nature of the reporter system and whether the reporter gene is in the form of DNA or RNA, but may include, but not be limited to, such elements as promoters, enhancers, translational control sequences, poly A addition signals, transcriptional termination signals and the like.

The terms "transform", "transfect", "transduce", shall refer to any method or means by which a nucleic acid is introduced into a cell or host organism and may be used interchangeably to convey the same meaning. Such methods include, but are not limited to, transfection, electroporation, microinjection, PEG-fusion, biolistic bombardment and the like.

A "clone" or "clonal cell population" is a population of cells derived from a single cell or common ancestor by mitosis.

A "cell line" is a clone of a primary cell or cell population that is capable of stable growth *in vitro* for many generations.

CRE-MEDIATED SITE SPECIFIC RECOMBINATION

The plastid genome of higher plants is present in 100-10,000 copies per cell. Incorporation of a selectable marker gene is essential to ensure preferential maintenance of the transformed plastid genome copies carrying useful genes with no selectable phenotype. However, once transformation is accomplished, maintenance of the marker gene is undesirable. In accordance with the present invention, a bacteriophage P1CRE-*loxP* site-specific recombination system is provided which is suitable for efficient elimination of marker genes from the plastid genome. The system exemplified herein has two components: a plastid tester strain carrying a cytosine deaminase (*codA*) transgene flanked by *lox* sites conferring sensitivity to 5-fluorocytosine and a nuclear CRE line carrying a nuclear-encoded, plastid-targeted CRE. Both the plastid tester (no CRE activity) and the nuclear CRE line (no *lox* sequence) were genetically stable. However, *codA* was eliminated at a very fast rate when the plastid-targeted CRE was introduced into the plastid tester strain by transformation or crossing. The gene for the nuclear-encoded CRE was subsequently separated from the transformed plastids by segregation in the seed progeny. Excision of *codA* by CRE was often accompanied by deletion of a plastid genome segment flanked by short directly repeated sequences. Removal of the antibiotic resistance marker from the transplastomic plants

eliminates the metabolic burden imposed by the expression of the selectable marker gene and should also improve public acceptance of the transgenic crops. Additional applications of the CRE-*lox* site-specific recombination system are activation of plastid gene expression by deletion or inversion of plastid genome sequences and induction of controlled cell death by deleting vital genes in the male reproductive tissue.

Although the use the CRE recombinase is exemplified herein, other prokaryotic and eukaryotic site-specific recombinases would be equally suitable for the elimination of the marker genes.

Recently, several prokaryotic and lower eukaryotic site-specific recombination systems have been shown to operate successfully in higher eukaryotes. In plant and animal cells functional site-specific recombination systems from bacteriophages P1 (Cre-*lox*) Mu (Gin-*gix*), and from the inversion plasmids of *Saccharomyces cerevisiae* (FLP-*frt*) (Morris et al. 1991; O'Gorman et al. 1991; Lichtenstein and Barrena 1993; Lyznik et al. 1993; Lyznik et al. 1995; Lyznik et al. 1996) and *Zygosaccharomyces rouxii* (R-*RS*). In each of these systems, no additional factor aside from the recombinase and target sequences is required for recombination. Reviewed in van Haaren and Ow, 1993. The CRE-*loxP* site-specific recombination system of bacteriophage P1 has been studied extensively *in vitro* and in *E. coli* (Craig 1988; Adams et al. 1992). Expression of the CRE protein (38.5 kDa) is sufficient to cause recombination between 34 bp *loxP* sites that consist of 13 bp inverted repeats separated by 8 bp asymmetric spacer sequence. If there are two *loxP* sites within a DNA segment, the result of the recombination reaction depends on the relative position of the recombination sites. If the recombination sites form a direct repeat, that if they

are in the same orientation, recombination results in deletion of the intervening DNA. If the recombination sites are in an inverted orientation, CRE-mediated recombination results in an inversion of the intervening DNA. The products of these reactions are shown in Fig. 1. The CRE site-specific recombination system has been employed for the elimination of nuclear genes in a number of eukaryotic systems, including higher plants (Dale and Ow 1991; Russell et al. 1992; Srivastava et al. 1999).

Before the present invention, the efficiency of CRE-mediated elimination of targeted plastid genes was unknown. To explore this system for this purpose, CRE-mediated elimination of the *codA* gene encoding cytosine deaminase (CD; EC 3.5.4.1) was assessed. Cytosine deaminase converts 5-fluorocytosine (5FC) into 5-fluorouracil (5FU), the precursor of 5-fluoro-dUMP. 5FC is lethal for CD-expressing cells due to irreversible inhibition of thymidylate synthase by 5-fluoro-dUMP (Beck et al. 1972). Cytosine deaminase is absent in plants. Expression of the bacterial *codA* in plastids renders cells sensitive to 5FC, while cells deficient in transgene expression are resistant (Serino and Maliga 1997). Thus, 5FC resistance could be used for positive identification of cells with CRE-induced *codA* deletion, even if such deletion events were relatively rare. The test system of the present invention incorporates a *codA* gene in the tobacco plastid genome between two directly oriented *lox* sites (>*codA*>). The transplastome was stable in the absence of CRE activity. However, highly efficient elimination of >*codA*> was triggered by introduction of a nuclear-encoded plastid-targeted CRE.

EXAMPLE 1

CRE-MEDIATED DELETION OF THE SELECTABLE PLASTID MARKER

Cre-mediated deletion of the selective plastid marker in the plastids of tobacco somatic cell is described in Example I. The selectable marker flanked by the lox sites is exemplified here by codA. However, it could be any other selectable and non-selectable marker gene, or any DNA sequence independent of information content flanked by lox sites in the palstid genome. Components of the test stystem are tobacco plants carrying a codA coding region flanked by lox sites (>codA>). A second component of the test system is a nuclear gene encoding a plastid targeted CRE-site specific recombinase. Deletion of a plastid encoded >codA> is achieved by introducing nuclear Cre into the nucleus of somatic (leaf) tobacco cells by Agrobacterium-mediated transformation. Alternatively, the nuclear encoded Cre gene may be introduced by fertilization with pollen of an appropriate activator-of-deletion strain. The nuclear Cre gene is subsequently removed by segregation in the seed progeny.

MATERIALS AND METHODS FOR THE PRACTICE OF EXAMPLE 1

The following materials and methods are provided to facilitate the practice of Example 1.

Plastid *codA* with direct *lox* sites.

The *codA* gene is contained in a *Sac*I-*Hin*dHIII fragment. The gene map is shown in Fig. 2. Prrn*lox*D (Seq. ID No. 4) is a plastid rRNA operon (*rrn16*) promoter derivative. It is contained in a *Sac*I-*Eco*RI fragment obtained by PCR using oligonucleotides 5'-GGGGAGCTCGCTCCCCCGCCGTCGTTCAATG-3' and 5'-GGGAATTCATAACTTCGTATAGCATACATTATACGAAGTTAT

GCTCCCAGAAATATAGCCA-3' as primers and plasmid pZS176 (progenitor of plasmid pZS197; Svab and Maliga 1993) as a template. The promoter fragment Prrn*lox*D contains a *lox* site at the 3' end adjacent to the *Eco*RI site. The *Eco*RI-*Nco*I fragment contains the ribosome binding site from plasmid pZS176. The fragment was obtained by annealing the complementary oligonucleotides 5'-AATTCGAAGCGCTTGGATACAGTTGTAGGGAGGGATC-3' and 5'-CATGGATCCCTCCCTACAACTGTATCCAAGCGCTTCG-3'. The *codA* coding region is contained in an *Nco*I-*Xba*I fragment (Serino and Maliga 1997). The TrbcL*lox*D (Seq. ID No. 5) is the *rbcL* 3'-untranslated region contained in an *Xba*I-*Hin*dIII fragment obtained by PCR using oligonucleotides 5'-GGTCTAGATAACTTCGTATAATGTATGCTATA CGAAGTTATAGACATTAGCAGATAAATT-3' and 5'-GGGGGTACCAAGCTTGCTAGATTTTGTATTTCAAATCTTG-3' and plasmid pMSK48 (Khan and Maliga 1999) as template. TrbcL*lox*D contains a *lox* site adjacent to the *Xba*I site in direct orientation relative to the *lox* site in the *codA* 5'UTR. The chimeric *PrrnloxD:codA:TrbcLloxD* gene was introduced into the tobacco plastid transformation vector pPRV111B (Zoubenko et al. 1994) as a *Sac*I-*Hin*dIII fragment to obtain plasmid pSAC48.

Plastid-targeted nuclear *cre* linked to a nuclear kanamycin resistance gene. Two plastid targeted nuclear *cre* genes were tested. The *cre* gene in *Agrobacterium* binary vector pKO27 and pKO28 encode the CRE recombinase at its N terminus translationally fused with the pea Rubisco small subunit (SSU) chloroplast transit peptide (Timko et al. 1985) and twenty two and five amino acids of the mature Rubisco small subunit, respectively. Both *cre* genes are contained in an *Eco*RI-*Hin*dIII fragment. The schematic map of the genes is shown in Fig. 3. The

P2' Agrobacterium promoter (Velten et al. 1984) (Sequence ID. No.9) is contained in an *Eco*RI-*Nco*I fragment. The P2' promoter fragment was obtained by PCR using oligonucleotides 5'-ccgaattcCATTTTCACGTGTGGAAGATATG-3'and 5'-ccccatggtaggatcctatCGATTTGGTGTATCGAGATTGG-3' as primers and plasmid pHC1 (Carrer et al. 1990) as template. PCR amplification introduced an *Eco*RI site at the 5' end and *Cla*I, *Bam*HI and a *Nco*I sites at the 3' end. A T introduced between the *Cla*I and the *Bam*HI sites eliminates an ATG and introduces an in-frame stop codon (Sriraman 2000). The Rubisco SSU transit peptides are included in *Bam*HI-*Nco*I fragments. The pKO27 fragment (Pea SSU-TP22; Sequence ID No. 7) was obtained by using oligonucleotides 5'-CCGGATCCAATTCAACCACAAGAACTAAC-3' and 5'-GGGGCTAGCCATGGCAGGCCACACCTGCATGCAC-3' as primers and plasmid pSSUpGEM4 as the template (Timko et al. 1985). The pKO28 fragment (Pea SSU-TP5; Sequence ID No. 6) was obtained by using oligonucleotides 5'-CCGGATCCAATTCAACCACAAGAACTAAC-3' and 5'-GGGGCTAGCCATGGTCAATGGGTTCAAATAGG-3' as primers and plasmid pSSUpGEM4 as the template (Timko et al. 1985). A pea SSU-TP with 23 amino acids of the mature polypeptide is shown in Sequence ID No. 8. The *cre* coding region included in a *Nco*I-*Xba*I fragment (Sequence ID No. 3) was obtained by PCR amplification using the Cre1 5'-GGGGAGCTCCATGGCTAGCTCCAATTTACT GACCGTACAC-3' and Cre2 5'-GGGTCTAGACTAATCGCCATC CTCGAGCAGGCGCACCATTGC-3' oligonucleotides as primers and DNA isolated from *Escherichia coli* strain BNN132 (ATCC number 47059) as template. The presence of cre gene in plant nuclear DNA was confirmed by PCR amplification with the Cre 1 and Cre3 oligonucleotides. The sequence of Cre3 oligonucleotide is 5'-TCAATCGATGAGTTGCTTC-3'. The *Agrobacterium nos* terminator (Tnos) is included in a

*Xba*I-*Hin*dIII fragment (Svab et al. 1990). The plastid targeted nuclear *cre* genes were introduced as *Eco*RI-*Hin*dIII fragments into the pPZP212 *Agrobacterium* binary vectors (Hajdukiewicz et al. 1994) to obtain plasmids pKO27 and pKO28 with twenty two and five amino acids of the mature Rubisco SSU. A schematic map of the *Agrobacterium* vectors is shown in Fig. 3.

Transgenic plants. Plastid transformation using the biolistic protocol, selection of transplastomic tobacco clones (RMOP medium, 500 mg/L spectinomycin dihydrochloride) and characterization of the transplastomic clones by DNA gel blot analysis was described (Svab and Maliga 1993). Transformation with *Agrobacterium* vectors pKO28 or pKO27 and regeneration of transformed tobacco plants has also been reported (Hajdukiewicz et al. 1994). Briefly, nuclear gene transformants were selected by kanamycin resistance on RMOP shoot regeneration medium containing 100 mg/L kanamycin and 500 mg/L carbenicillin. Kanamycin resistance of the shoots was confirmed by rooting on plant maintenance (RM) medium containing 100 mg/L kanamycin. Testing of 5FC cytotoxicity was carried out on RMPO medium according to published procedures (Serino and Maliga 1997).

Transplastomic tobacco plants with a *codA* gene flanked by direct *lox* sites.

Plastid transformation vector pSAC48 carries a *codA* gene in which two lox sites flank the coding region in a direct orientation. If the *codA* coding region is deleted via the *lox* sites, a *lox* site flanked by the promoter (Prrn) and terminator (TrbcL) are left behind. The selective marker in pSAC48, a pPRV111B vector

derivative, is a spectinomycin resistance (*aadA*) gene (Fig. 2). Transformation with plasmid pSCAC48 yielded a number of independently transformed transplastomic lines, of which four were purified to the homoplastomic state: Nt-pSAC48-21A, Nt-pSAC48-16C, Nt-pSAC48-16CS and Nt-pSAC48-9A. These lines are considered identical other than they have been generated independently. A uniform population of transformed plastid genomes in the transplastomic plants was verified by DNA gel blot analysis (see below).

Nuclear-encoded plastid-targeted Cre genes.

To activate deletion of the plastid >codA> gene we introduced an engineered *cre* gene into the nucleus of the transplastomic lines encoding a plastid-targeted CRE. Targeting of nuclear-encoded plastid proteins is by an N-terminal transit peptide (TP) cleaved off during import from the cytoplasm into plastids (Soll and Tien, 1998). To ensure plastid targeting of the CRE recombinase, it was translationally fused with the Rubisco small subunit (SSU) transit peptide (Timko et al. 1985). Therefore, the product of the protein fusion is SSU-TP-CRE. Efficiency of import of chimeric proteins depends on the size of mature protein N-terminus incorporated in the construct (Wasmann et al. 1986; Lubben et al. 1989). Two chimeric *cre* genes (*Ssu-tp-cre*) were prepared, one with 5 (vector pKO28) and one with 22 (plasmid pKO27) amino acids of the mature SSU N-terminus, encoding SSU-TP5-CRE and SSU-TP22-CRE, respectively. These genes are also referred to as *Cre1* and *Cre2*, respectively (Table 1). The *cre* genes were expressed in the P2' promoter and Tnos terminator cassettes in the *Agrobacterium* pPZP212 binary vector which carries kanamycin resistance (*neo*) as a selectable marker (Fig. 3).

Tobacco plant transformed with *Ssu-tp5-cre* (pKO37) and *Ssu-tp22-cre* (pKO36) were also obtained. In these plants the nuclear *cre* is expressed from the cauliflower mosaic virus 35S promoter (Seq. ID No. 10; Timmermans et al. 1990).

Line	Plastid genotype[a]	Nuclear marker	
Wild-type	*trnV+ aadA- codA-*		
Nt-pSAC48-21A Nt-pSAC48-16C	*trnV+ aadA+ codA+*		
Cre1-1	*trnV+ aadA+ codA-* *trnV- aadA- codA-*	*neo*	
Cre1-2	*trnV+ aadA+ codA-* *trnV- aadA- codA-*	*neo*	
Cre1-3	*trnV+ aadA- codA-*	*neo*	
Cre1-4	*trnV- aadA- codA-*	*neo*	
Cre1-10	*trnV- aadA- codA-*	*neo*	
Cre2-1	*trnV+ aadA+ codA-*	*neo*	
Cre2-2	*trnV+ aadA+ codA-* *trnV+ aadA*+ codA-* *trnV- aadA- codA-*	*neo*	
Cre2-3	*trnV+ aadA+codA+* *trnV+ aadA+ codA-* *trnV+ aadA*+ codA-* *trnV- aadA- codA-*	*neo*	
Cre2-4	*trnV+ aadA+ codA-*	*neo*	
Cre2-5	*trnV+ aadA+ codA-*	*neo*	
Cre2-10	*trnV+ aadA+ codA-* *trnV- aadA- codA-*	*neo*	
Cre1-100	*trnV+ aadA- codA-*	*neo*	
Cre2-100	*trnV+ aadA- codA-*	*neo*	
Cre2-200	*trnV+ aadA- codA-*	*neo*	
Cre2-300	*trnV+ aadA- codA-*	*neo*	

[a]Presence or absence of plastid gene is indicated by + or -. Since the plastid trnV gene is deleted in some of the lines, the wild-type plastid genotype is *trnV+ aadA- codA-*.

Deletion of *codA* from the plastid genome in somatic

c lls.

To test the efficiency of CRE-mediated deletion in somatic cells, the *Ssu-tp-cre* genes were introduced into the nucleus of the transplastomic >codA> lines by cocultivation of *Agrobacterium* and tobacco leaf disks. Plants representing 11 individual *Ssu-tp-cre* insertion events have been characterized. Five lines (Cre1-derivatives) were obtained by transformation with *Ssu-tp5-cre* gene (vector pKO28) and six lines (Cre2-derivatives) were obtained by transformation with the *Ssu-tp22-cre* (vector pKO27) (Table 1).

Deletion of *codA* was first tested in a DNA sample taken from one leaf of eleven kanamycin resistant shoots representing an individual integration event of the nuclear *Cre* gene. Subsequently, 4 to 7 additional leaves were sampled from six shoots to confirm that the result of the analysis is typical for the plant.

The initial DNA samples were first screened for the loss of *>codA>* by PCR using the O1/O2 primer pair complementary to sequences in the *aadA* coding region N terminus and the *codA* promoter (Fig. 4A). Amplification with these primers yields a ~0.7-kb fragment if >codA> is deleted and a ~2.0-kb fragment if the >codA> gene is still present. Ethidium bromide stained gels of PCR products in Fig. 5 indicate complete loss of *>codA>* in each of the samples. A perfect, reconstituted *lox* site between Prrn and TrbcL was confirmed in eight clones by PCR amplification of the region with primers O1/O4 from the same DNA samples and direct sequencing of the amplification product with primer O2 (not shown). In two clones (Cre1-4, Cre1-10) a fragment is missing due to deletion of *aadA* alongside with *codA* (see below).

Plastid genome structure in the initial DNA sample was determined by gel blot analysis of *ApaI-EcoRV* digested

total cellular DNA. The probes were the plastid targeting region and the *aadA* and *codA* coding regions. The DNA gel blots are shown in Fig. 6. The maps of the parental genomes and deletion derivatives that help to interpret these genomes are shown in Fig. 4. In the plastid tester strains expressing no CRE (Nt-pSAC48-21A, Nt-pSAC48-16C) all three probes hybridized to the same 4.9-kb DNA fragment consistent with both *codA* and *aadA* being present in all the plastid genome copies. In the SSU-TP-CRE expressing plants no 4.9-kb fragment was detectable indicating the dramatic speed by which the >*codA*> gene was eliminated from the plastid genome. CRE-mediated deletion of >*codA*> via the *lox* sites yielded the 3.6-kb fragment detected in nine of the eleven clones. The 3.6-kb fragment was the only product detected in four clones, and was present in a heteroplastomic population in five clones. Unanticipated was formation of a 1.4-kb *Apa*I-*Eco*RV fragment in five clones. DNA gel blot analysis confirmed that this fragment lacks both *codA* and *aadA*, and is smaller than the wild type *Apa*I-*Eco*RV fragment (1.9-kb). Direct sequencing of PCR products in this region confirmed deletion of *codA*, *aadA* and *trnV* by homologous recombination *via* the duplicated *Prrn* promoter regions. One of the *Prrn* promoters is driving *codA*, the other is upstream of the rRNA operon at its native location. Deletion of *trnV* is the reason why the *Apa*I-*Eco*RV fragment derived from this region (1.4-kb) is smaller than the wild-type fragment (1.9-kb).

The initial DNA samples were taken from one leaf of a plant obtained by rooting the shoot obtained after transformation with the *Ssu-tp-cre* genes. To confirm that the DNA samples extracted from the leaf were typical for the plant, we have sampled several more

leaves from the same plants (Fig. 7). In four clones *codA* was excised by CRE via the *lox* sites, and the shoots were homoplastomic for the deleted genome. Two of these, Cre1-3 and Cre2-4 were further characterized by testing seven and four additional leaves of the same plants, respectively. DNA gel blot analysis of these samples confirmed a uniform deletion of >codA> from all genome copies. These plants are the desired final products carrying the desired plastid transgenes and lacking the undesirable selective marker. These plants and their progeny can be used directly for the production of recombinant proteins as they are free from the selectable marker gene. Furthermore, these plants are a source of engineered chloroplasts for introduction into breeding lines by sexual crossing. The seed progeny of the plants is segregating for the *Ssu-tp-cre* activator gene. Plants with the desired chloroplasts but lacing the activator gene can be identified by PCR testing for *cre* sequences. Alternatively, individuals lacking *cre* can be identified in the seed progeny by sensitivity to kanamycin, since the Ssu-tp-cre genes in the pKO27 and pKO28 Agrobacterium vectors are physically linked to kanamycin resistance (*neo* gene; Fig. 3). In two clones, Cre1-4 and Cre1-10, deletion of *trnV* (encoding tRNA-Val^{GAC}), *aadA* and *codA* occurred by homologous recombination *via* the duplicated Prrn promoter region. The Cre1-10 plant is homoplastomic for the deletion based on probing seven additional leaves (Fig. 7). Apparently, the one remaining *trnV* gene encoding tRNA-Val^{UAC} is sufficient for the translation of all valine codons, or there is import of tRNA-Val^{GAC} from the cytoplasm. In the Cre1-4 clone some of the leaves (two out of four) contained residual genome copies with *trnV* and *aadA*.

In five clones the initial DNA samples contained

more than one type of plastid genome copies. Mixed populations of plastid genome populations were confirmed in all parts of the plants by testing additional leaves (Fig. 7). Genetically stable *codA* deletion lines can be obtained from these heteroplastomic plants by testing plants regenerated from single somatic cells or individual seedlings in a segregating seed progeny.

Deletion of *codA* from the plastid genome in the seed progeny.

CRE-mediate deletion of the negative plastid marker *codA* in somatic cells was described in the previous section. Deletion of the plastid marker gene in the somatic cells of the transplastomic plants, without going though a sexual cycle, is highly desirable to accelerate the production of marker-free transplastomic plants. However, this approach is feasible only if there is a system for tissue culture and plant regeneration from somatic cells. Such system is unavailable for the economically important cereal crops rice and maize. As an alternative to transformation of somatic cells, we developed CRE activator lines carrying a nuclear-encoded plastid-targeted Cre to be used as the source of Cre gene when used as a pollen parent. The tobacco CRE activator lines were obtained by transforming the nucleus of wild-type plants with SSU-TP-CRE constructs. Lines in which the Cre is linked to a nuclear kanamycin resistance gene in a wild-type cytoplasm are Cre1-100, Cre-2-100, Cre2-200 and Cre2-300 (Table 1).

To activate deletion of >*codA*> in the seed progeny, tester plants Nt-pSAC48-21A and Nt-pSAC48-16C were emasculated to prevent self fertilization, and fertilized with pollen from the Cre2-200 and Cre2-300 activator lines. The activator lines are primary transgenic plants (T_0) segregating for the *Ssu-tp-cre*

gene. Therefore, a proportion of the seed progeny derived from the cross will have the activator genes while others will not. If the *codA* gene is present, the O1/O2 primer pair marked in Fig. 4 amplifies a 2.0-kb fragment. If the *codA* gene is absent, the same primers will amplify a 0.7-kb fragment. PCR analysis shown in Fig. 8 confirmed CRE-mediated deletion of >*codA*> in seedlings. The Cre1-100, Cre2-100 and Cre2-300 activator lines are apparently expressing CRE efficiently, indicated by the presence of only of the 0.7-kb fragment in seedlings carrying the nuclear *cre* gene. In seedlings with no *cre* sequence the same primers amplified the 2.0-kb *codA*-containing fragment. Interestingly, cre+ seedlings from the cross with Cre2-200 contained a mixed population of *codA* containing (2.0-kb) and *codA*-deleted (0.7-kb) fragments indicating less efficient CRE-induced deletion of >codA>. Thus, expression level and tissue specificity of the two nuclear *Ssu-tp22-cre* genes are characteristic for the individual transformation events. CRE activity of Cre1-100, Cre2-100 and Cre2-300 activator lines is more suitable for rapid elimination of >codA> in a cross than the Cre2-200 line.

It is undesirable to maintain the Ssu-tp-cre activator genes in the production lines. However, these are encoded in the nucleus, and can be separated from the transgenic chloroplasts in the next seed progeny. Linkage of *Ssu-tp-cre* to the nuclear kanamycin resistance gene facilitates identification of seedlings lacking *cre* in a segregating seed population.

CRE site-specific recombinase for deletion of plastid DNA sequences. Biolistic transformation of tobacco leaves always yields shoots containing a mixed population of plastid genome copies. A mixed population

of plastid genome copies is determined by DNA gel blot analysis (Carrer et al. 1993; Svab and Maliga 1993; Carrer and Maliga 1995) and can be visualized in UV light when expressing the green fluorescence protein in plastids (Khan and Maliga 1999). Homoplastomic, genetically stable plants are obtained during a second cycle of plant regeneration from the leaves of the regenerated plants or in the seed progeny. The cells of the >*codA*> tester strains carry a uniform population of plastid genome copies. Thus, the *Ssu-tp-cre* is introduced into the nuclear genome of a cell that is homoplastomic for >*codA*>. It was expected that the regenerated shoots would contain a mixed population of plastid genome copies. Instead, all plastid genome copies lack >*codA*>, an evidence for the enormous selection pressure by CRE activity against plastid genome copies that carry two *lox* sites. It is important that deletion of >*codA*> occurs in the absence of selection against >codA> by exposure to 5-fluorocytosine. Virtually complete elimination of >codA> may also be obtained when CRE activity is introduced by crossing, using pollen of an appropriate deletion activator strain. Deletion of the selectable marker in somatic cells is the preferred choice over elimination of the marker in the seed progeny. The most important advantage is time saving. Introduction of Ssu-tp-cre into the nucleus of somatic cells requires only three to six weeks; Ssu-tp-cre segregates out in the first seed progeny. In contrast, introduction and elimination of Ssu-tp-cre takes one additional seed progeny, about three months.

Interestingly, genome copies with one *lox* site or no *lox* site (wild-type) are stable in CRE-expressing cells. Instability of genomes with two *lox* sites may be due to formation of linear ends during the excision

process. The linear ends may then re-circularize by homologous recombination via the Prrn promoter sequences yielding the *trnV-aadA-codA* deletion derivatives.

CRE engineering. Although CRE is a prokaryotic protein, it naturally carries a nuclear localization signal (NLS) that targeted a CRE-GFP fusion protein to the nucleus in mammalian cells. The NLS sequences overlap the DNA binding regions and the integrity of this region is important for DNA recombinase activity (Le et al. 1999). We targeted the newly-synthesized TP-CRE protein to plastids using a plastid-targeting transit peptide (TP). The TP is localized at the N terminus of plastid proteins and is cleaved off during import from the cytoplasm into plastids (Soll and Tien, 1998). Therefore, we translationally fused a plastid transit peptide with CRE to direct its import from the cytoplasm to plastids. Translational fusion yielded a protein with an N-terminal plastid targeting signal and an internal nuclear localization signal. Efficient CRE-mediated deletion of plastid-encoded *codA* genes indicates targeting of SSU-TP-CRE to plastids. When two potential targeting sequences are present, in general one of them out-competes the other (Small et al. 1998). N-terminal organelle targeting sequences normally dominate the second internal localization signal. For example, the 70-kDa heat shock protein of watermelon cotyledons that carry N-terminal plastidal and internal glyoxysomal targeting sequences are exclusively targeted to plastids. Proteins are localized to glyoxysomes only in the absence of the plastidal presequence (Wimmer et al. 1997). The tRNA modification enzymes contain information for both mitochondrial (N-terminal extension) and nuclear targeting. The enzyme with the N-terminal extension is targeted to mitochondria and only the short

form lacking the N-terminal extension is targeted to the nucleus (Small et al. 1998). It was fortunate, that the Rubisco SSU N-terminal transit peptide dominated the CRE nuclear localization signals and the TP-CRE fusion protein was directed to plastids (chloroplasts).

A second property that is important for the present invention is maintenance of recombinase activity when CRE is fused with proteins or peptides at its N and C termini. N-terminal fusion of CRE with the *E. coli* maltose binding protein did not interfere with recombinase function (Kolb and Siddell 1996). CRE was also shown to accept a C-terminal fusion with GFP (Le et al. 1999) as well as an 11-amino-acid epitope to the herpes simplex virus (HSV) glycorpotein D coat protein. The epitope tag facilitates detection of CRE expression *in vitro* and *in vivo* using immunofluorescent labeling with a commercially available antibody (Stricklett et al. 1998). Apparently, the five and 22 amino acids that are left behind after processing of the SSU-TP5-CRE and SU-TP22-CRE proteins did not interfere with CRE function.

Dominant negative selection markers for positive identification of deletion derivatives. A practical application of the present invention is the removal of selectable marker genes from the transformed plastid genome. In tobacco, the excision process mediated by the CRE constructs described herein is so efficient that the >codA> deletion derivatives can be identified in the absence of 5FC selection. However, in other crops CRE-mediated excision of marker genes may be less efficient. In these species, the positive selective marker (*aadA*) may be fused with a dominant negative selective marker using linker peptides as described in the literature (Khan and Maliga 1999) or the positive and negative

marker genes may be combined in a dicistronic operon (Staub and Maliga 1995). Dominant negative selection markers allow normally non-toxic compounds to be used as toxic agents, so that cells which express these markers are non-viable in the presence of the compound, while cells that don't carry them are unaffected.

For example, cytosine deaminase is absent in plants. Expression of *codA*, encoding cytosine deaminase (CD; EC 3.5.4.1), in plastids renders tissue culture cells and seedlings sensitive to 5FC, facilitating direct identification of clones lacking this negative selective marker (Serino and Maliga 1997). Cytosine deaminase converts 5-fluorocytosine (5FC) into 5-fluorouracil (5FU), the precursor of 5-fluoro-dUMP. 5FC is lethal for CD-expressing cells due to irreversible inhibition of thymidylate synthase by 5-fluoro-dUMP (Beck et al. 1972). We have found that seedlings and plant tissues expressing >*codA*> were sensitive to 5FC. Seedlings lacking *codA* could be readily identified by 5FC resistance. Thus, the constructs described here are suitable to express cytosine deaminase at sufficiently high levels to be useful to implement a negative selection scheme.

Alternative negative selective markers can be obtained by adaptation of substrate-dependent negative selection schemes described for nuclear genes. Such negative selection schemes are based on resistance to indole, napthyl, or naphtalene acetamide (Depicker et al. 1988; Karlin-Neumann et al. 1991; Sundaresan et al. 1995), chlorate (Nussaume et al. 1991), kanamycin (Xiang and Guerra 1993) and 5-fluorocytosine (5FC) (Perera et al. 1993; Stougaard 1993).

EXAMPLE 2

Cr -MEDIATED INVERSION OF PLASTID DNA SEQUENCES

If the lox sites in bacteria are in an inverted orientation, CRE-mediated recombination results in an inversion of the intervening DNA. We have tested, whether the CRE-mediated inversion reaction also occurs in plastids of higher plants containing DNA sequences flanked by inverted lox sites. This was assessed using a kanamycin-resistance (>neo<) coding region in an inverted orientation relative to the promoter (Fig. 9). In this construct the non-coding strand *of neo is* transcribed and the plants are kanamycin sensitive. The *>neo<* coding region is flanked by inverted lox sites. CRE-mediated inversion of the sequences reverses *neo* orientation resulting in the transcription of the sense strand and expression of kanamycin resistance. Inversion of the plastid-encoded *>neo<* coding region may be achieved by multiple approaches. One approach is to introduce a nuclear Cre into the nucleus of somatic tobacco cells, e.g., leaf, by *Agrobacterium*-mediated transformation. A second approach is introduction of the nuclear-encoded Cre gene by fertilization with pollen of an appropriate activator-of-inversion strain. Additional approaches are to provide CRE-activity via the incorporation of chemically inducible promoter into the construct, or to transiently express CRE from a nuclear of chloroplast construct.

MATERIALS AND METHODS FOR THE PRACTICE OF EXAMPLE 2

Plastid neo **gene with inverted lox sites.** The neo gene is contained in a *SacI-HindHIII* fragment. The gene map is shown in Fig. 8. PrrnloxI (Seq. ID No. 1) is a plastid rRNA operon (rrn16) promoter derivative. It is contained in a *Sac*I-*Xba*I fragment obtained by PCR using oligonucleotides 5'-ggggagctcGCTCCCCCGCCGTCGTTCAATG-3' and 5'-ggtctagataacttcgtatagcatacattatacgaagttatGCTCCC AGAAATATAGCCA-3' as primers and plasmid pZS176

(progenitor of plasmid pZS197; Svab and Maliga 1993) as a template. The promoter fragment Prrn*lox*I contains a *lox* site at the 3' end adjacent to the *Xba*I site. The *neo* coding region is contained in an *Nco*I-*Xba*I fragment derived from plasmid pHC62. The *neo* sequence in plasmid pHC62 is identical with the *neo* sequence shown in Fig. 28B, US Patent 5,877,402. The *Eco*RI-*Nco*I fragment contains the ribosome binding site from plasmid pZS176. The fragment was obtained by annealing the complementary oligonucleotides 5'-AATTCGAAGCGCTTGGATACAGTTGTAGGGAGGGATC-3' and 5'-CATGGATCCCTCCCTACAACTGTATCCAAGCGCTTCG-3'. The TrbcL*lox*I (Seq. ID No. 2) is the *rbcL* 3'-untranslated region contained in an *Eco*RI-*Hin*dIII fragment obtained by PCR using oligonucleotides 5'-gggaattcataacttcgtatagcatacat tatacgaagttatAGACATTAGCAGATAAATT-3' and 5'-gggggtaccaagcttgCTAGATTTTGTATTTCAAATCTTG-3' and plasmid pMSK48 (Khan and Maliga 1999) as template. TrbcL*lox*I contains a *lox* site adjacent to the *Eco*RI site in an inverted orientation relative to the *lox* site in Prrn*lox*I. The chimeric *PrrnloxI*:*neo*:*TrbcLloxI* gene was introduced into the tobacco plastid transformation vector pPRV111B (Zoubenko et al. 1994) as a *Sac*I-*Hin*dIII fragment to obtain plasmid pSAC38.

Plastid-targeted nuclear *cre* linked to a nuclear gentamycin resistance (*aacC1*) gene. The plastid targeted nuclear *cre* genes were introduced as *Eco*RI-*Hin*dIII fragments into the pPZP222 *Agrobacterium* binary vectors which carry a plant-selectable gentamycin resistance gene (Hajdukiewicz et al. 1994) to obtain plasmids pKO30 and pKO31 with twenty two and five amino acids of the mature Rubisco SSU. The map of the Agrobacterium vectors is identical with the one shown in Fig. 3. other than

they carry a gentamycin resistance gene.

Transplastomic tobacco plants with a *neo* gene flanked by inverted *lox* sites.

Plastid transformation vector pSAC38 with the inverted >*neo*< gene is shown in Fig. 9. The inverted >*neo*< gene was introduced into plastids by selection for spectinomcyin resistance (aadA) encoded in the vector. Two independently transformed lines were purified to the homoplastomic state: Nt-pSAC38-9A and Nt-pSAC38-10C. The homoplastomic state was confirmed by DNA gel blot analysis.

Nuclear-encoded plastid-targeted Cre genes.

Plant activator lines in which *Ssu-tp*-cre is linked to a nuclear kanamycin resistance gene have been described in Example 1. The plastid marker to test CRE-activated inversion described in Example 2 utilizes a kanamycin resistance gene. Kanamycin resistance conferred by the plastid gene due to CRE-mediated inversion could not be distinguished from kanamycin resistance conferred by the marker gene of the Agrobacterium binary vector that was used to introduce the nuclear *cre*. Therefore, we have constructed activator strains in which Ssu-tp-cre is linked to gentamycin resistance. The *Ssu-tp22-cre* gene linked to the nuclear gentamycin resistance is the Cre3 strain and the *Ssu-tp5-cre* gene linked to gentamycin resistance is the Cre4 strain.

Inversion of >*neo*< in the plastid genome of somatic cells.

The nuclear cre genes were introduced into the

chloroplast >*neo*< tester strains by cocultivation of tobacco leaves with the Agrobacterium strains and selection for gentamycin resistance (100 mg/L). Digestion of total cellular DNA with BamHI and probing with the plastid targeting region (ApaI-EcoRV fragment, Fig. 4) hybridizes to 1.8-kb and a 3.8-kb fragments in the parental Nt-pSAC38-10C lines (Fig. 10). Activation by CRE in lines Cre3-3 and Cre4-5 created a mixed population of >*neo*< genes representing the original and inverted orientations detected as the original 3.8-kb and 1.8-kb and the newly created 4.6-kb and 0.9-kb hybridizing fragments. Lines carrying the *cre* and an approximately wild-type size fragment are *aadA-neo* deletion derivatives, similar to those shown in Fig. 4. Thus, it appears that CRE mediated inversion via *lox* sites creates increased local recombination frequencies that leads to deletion of the transgenes via the short direct repeats of Prrn promoters.

Controlling inversion via *lox* sites by CRE activity.

Here we describe constructs for CRE-mediated inversion of plastid genome segements flanked by inverted *lox* sites. Inversion of the sequences is independent of the encoded genetic information and relies only on CRE activity. CRE activity may be provided transiently, by expression in plastids from plastid signals described in US patent 5,877,402, or from nuclear genes encoding a plastid-targeted CRE. Such plastid-targeted CRE constructs are described in Example 1, for example the *Ssu-tp5-cre* or *Sssu-tp22-cre* genes. Alternative approaches to provide CRE activity are stable incorporation of a plastid-targeted nuclear *Cre* into the nucleus of somatic (leaf) cells by *Agrobacterium*-mediated, PEG induced or biolistic

transformation or by fertilization with pollen from a transformed plant. The Agrobacterium P2 promoter and cauliflower mosaic virus 35S promoter exemplified here are constitutive promoters. Regulated expression of CRE may be important for certain applications. Developmentally timed expression may be obtained from promoters with tissue specific activity. Regulated expression of CRE may be obtained from chemically induced nuclear gene promoters responding to elicitors, steroids, copper or tetracycline (reviewed in; Gatz et al. 1992; Mett et al. 1993; Aoyama and Chau 1997; Gatz 1997; Martinez et al. 1999; Love et al. 2000) and described in US patent 5,614,395.

Controlled expression of deleterious gene products

There are a variety of valuable heterologous proteins that interfere with plastid metabolism. For example, certain proteins may be inserted into photosynthetic membranes and interfere with photosynthesis. This problem can be circumvented by first growing the plants to maturity, then activating production of the deleterious protein by chemically inducing CRE expression. CRE, in turn, will make the gene expressible by *lox*-mediated inversion of the coding region.

The molecular tools necessary for the construction of such plastid genes are described in present application. In case of the monocistronic inversion vector the gene of interest (*goi*) is flanked by inverted *lox* sites and is introduced by linkage with *aadA* (Fig. 12). The selectable marker (*aadA*) coding region is the first reading frame, and is expressed from the promoter. The *goi* reading frame is the second coding region, and it is not expressed as it is in an inverted orientation relative to the promoter. Expression of *goi* is induced

by CRE-mediated inversion of the *goi* coding region, as described for >*neo*< in Example 2 and is shown in Fig. 12.

The dicistronic *lox* inversion vector is shown in Fig. 13. In this case the inverted lox sites flank both *aadA* and *goi*. The selectable marker (*aadA*) coding region is expressed from the promoter. The *goi* reading frame is not expressed as it is in an inverted orientation relative to the promoter. Expression of *goi* is induced by CRE-mediated inversion of the *aadA-goi* containing region that results in simultaneous expression of *goi* and inactivation of *aadA*.

The presence of two *lox* sites may destabilize the plastid genome that leads to CRE-independent deletion of plastid genome sequences. However, it appears that CRE activity by itself is not mutagenic, and the plastid genomes are stable if only one *lox* site is present. Mutant *lox* sites that are efficiently excised but recombine into excision resistant sites have been described (Hoess et al. 1982; Albert et al. 1995). Such *lox* sites would mediate efficient inversion, but the new *lox* sites would be resistant to additional cycles of CRE activation. Providing only a short burst of CRE activation using a chemically induced promoter could further refine the expression system.

EXAMPLE 3

CRE-MEDIATED DELETION TO OBTAIN MARKER FREE TRANSPLASTOMIC PLANTS AND FOR HIGH LEVEL EXPRESSION OF THE RECOMBINANT PROTEINS

Plastid *loxP* vectors in this section are described for CRE-mediated excision of selective markers in transplastomic plants. Since excision of sequences

between directly oriented *lox* sites is very efficient, variants of the same vectors can be used for CRE-activated expression of recombinant proteins. A family of plastid vectors with suitably positioned *lox* sites is shown schematically in Fig. 14 through Fig. 17.

The map of the basic tobacco plastid *lox* deletion vector is shown in Fig. 14. It contains (a) two directly oriented *lox* sites separated by a unique *Bgl*II cloning site and (b) an adjacent polycloning site. These sequences (Seq. ID No. 11) are inserted into the *Sca*I site plastid repeat vector pPRV100 (US Patent 5,877,402; Zoubenko et al. 1994). Suitable marker genes (*aadA, neo or kan, bar,* glyphosate resistance, bromoxynil resistance) for insertion into the BglII site have been described in US Patent 5,877,402, WO 00/07421 and WO 00/03022.

The map of the tobacco plastid *lox* >*aadA*> deletion vector is shown in Fig. 15. It is the basic *lox* deletion vector with an *aadA* gene cloned into the *Bgl*II sites oriented towards the *rrn* operon.

Maps of constitutive *lox* dicistronic deletion vectors are shown in Fig. 16 through Fig. 18. This dicistronic design enables simultaneous expression of both the first and the second open reading frames. The selectable marker designed for excision may be encoded in the first (Fig. 16) or second (Fig. 17, Fig. 18) open reading frames. Since a minimally 34 bp *lox* site is located between the two reading frames, both the marker gene (*aadA*) and the gene of interest have their own leader sequence to facilitate translation (Fig. 16, Fig. 17). Translational coupling may also be feasible if the *lox* site is incorporated in the marker gene coding region N terminus (Fig. 18). DNA sequence of promoter-*lox* constructs shown in Figs. 16 is set forth in Seq. ID

No. 1. Promoters and promoter-leader combinations suitable to promote high-level protein expression in plastids are described in European Patent Applications WO 00/07421, WO 97/06250 and WO 98/55595. Sequences suitable for directly oriented *lox* sites are given in Seq. ID No. 11. Translational coupling between a gene of interest and the downstream *aadA* is shown in Fig. 18. There are multiple ways of achieving translational coupling between adjacent genes (Baneyx 1999). One approach is incorporation of a properly spaced ribosome binding-site in the upstream gene's coding region (Schoner et al. 1986; Omer et al. 1995). An example for a suitable sequence directly upstream of the translation initiation codon (ATG) would be G-GAG-GAA-TAA-CTT-ATG. A specific example for the use of the sequence is translational coupling between a *bar* (suitable source described in European Patent Application WO 00/07421) and a downstream *aadA* are given in Seq. ID No. 12. Note SalI site downstream of AUG incorporated to facilitate engineering the BglII-SalI region and the directly oriented *lox* sites in the *aadA* coding region and downstream of *aadA*. The sequence is given for a BglII-SpeI fragment. The BglII site is within the *bar* coding region; the *Spe*I site is downstream of the second *lox* site, as marked in Fig. 18. If a C-terminal extension to create a ribosome binding site is unacceptable, a suitable sequence may be obtained by silent mutagenesis of the coding region at the third codon position. Variants of plastid ribosome binding sites have been catalogued (Bonham-Smith and Bourque 1989)

A tobacco inducible *lox* deletion vector is shown in Fig. 19. The marker gene (*aadA*) is encoded in the first reading frame, followed by a silent *goi* lacking the translation initiation codon (ATG) and the 5'

untranslated leader. Expression of the *goi* frame is triggered by *aadA* excision that results in translational fusion of the *aadA* N-terminal region with the *goi*. After aadA excision the *goi* mRNA is translated from the *aadA* translation control signals, the 5' UTR and AUG. DNA sequence of the SacI-NheI fragment is given in Seq. ID. No. 13. The Prrn promoter-*atpB* translational control region is described in European Patent Application WO 00/07421. The *aadA* construct has two directly-oriented *lox* sites: one in the coding region N-terminus and one downstream of *aadA* to facilitate CRE-mediated excision of the marker gene.

EXAMPLE 4

DELETION OF VITAL PLASTID GENES TO OBTAIN CYTOPLASMIC MALE STERILITY

US Patent 5,530,191 provides a cytoplasmic male sterility (CMS) system for plants, which is based on modification of the plastid genome. The CMS system comprises three transgenes: a "plastid male sterility" gene that causes plastid and cellular disablement of the anther tissue, and two nuclear genes that regulate the expression of the plastid gene. An important feature of the system is developmentally timed cellular death based on the expression, or the lack of the expression, of a plastid gene. As one specific approach to induce developmentally timed ablation of anther tissue we describe CRE-mediate excision of essential plastid genes *via* directly oriented *lox* sites.

The number of genes encoded by the plastid genome is about 120. Some of the genes are non-essential and may be inactivated by targeted gene disruption without a major phenotypic consequence. Good examples are the plastid *ndh* genes (Burrows et al. 1998; Shikanai et al.

1998) or the *trnV* gene the deletion of which has been described in Example 1. Excision of these genes is unlikely to cause cell ablation. The photosynthetic genes are essential for survival under field conditions. However, pigment deficient, non-photosynthetic plants can be maintained as long as they are grown on a sucrose-containing medium, or are grafted onto photosynthetically active wild-type (green) plants (Kanevski and Maliga 1994). Some of the house-keeping genes, such as the genes encoding the plastid multisubunit RNA polymerase are essential for photosynthetic growth, but not for survival (Allison et al. 1996). Thus, deletion of these genes is not suitable to trigger cell death. Only a relatively small number of plastid genes have proven to be essential for viability. The essential nature of the genes was recognized by the lack of homoplastomic cells in gene disruption experiments indicating that the loss of these genes results in cellular death. Cellular death due to lack of plastid function is understandable, as plastids are the site of the biosynthesis of amino acids, several lipids and are required for nitrate assimilation. Examples of plastid genes essential for cellular survival are the *clpP* protease subunit gene (Huang et al. 1994), *ycf1* and *ycf2*, the two largest plastid-encoded open reading frames (Drescher et al. 2000).

To induce cellular death by CRE-mediated excision, directly oriented *lox* sites can be incorporated in the plastid genome flanking essential genes, as shown for *clpP* in Fig. 20. The *clpP* gene has two large introns (807 bp and 637 bp) and the region can be conveniently cloned as a SalI-SphI fragment. The selectable marker *aadA* is inserted into a *KpnI* restriction site created by PCR mutagenesis downstream of *clpP* Exon 3, oriented towards *rps12* Exon I. One of the *lox* sites is

engineered next to the *aadA* gene, the second *lox* site is inserted in Intron I. Cellular death is induced by activation of the nuclear *Cre* gene as described in US Patent 5,530,191. It is necessary to use a selective marker, such as *aadA* to introduce the *lox* sites into the plastid genome. The *aadA* gene can subsequently eliminated using a second, independent site specific recombinase such as FRT via the *frt* sites engineered into the transformation vector shown in Fig. 20.

Alternative targets for CRE-mediated deletion in a CMS system are the essential ribosomal protein genes such as *rpl23*, the ribosomal RNA operon (for insertion sites see; Staub and Maliga 1992; Zoubenko et al. 1994) and the *ycf1* and *ycf2* genes (Drescher et al. 2000)

The following sequences are referred to throughout the specification and facilitate the practice of the present invention.

SEQ. No. 1: PrrnloxI. sequence

gagctcGCTCCCCCGCCGTCGTTCAATGAGAATGGATAAGAGGCTCGTGGGATTGA
CGTGAGGGGGCAGGGATGGCTATATTTCTGGGAGCataacttcgtataatgtatgc
tatacgaagttatctaga

SEQ. No. 2: TrbcLloxI. sequence

gaattcataacttcgtatagcatacattatacgaagttatAGACATTAGCAGATAA
ATTAGCAGGAAATAAAGAAGGATAAGGAGAAAGAACTCAAGTAATTATCCTTCGTT
CTCTTAATTGAATTGCAATTAAACTCGGCCCAATCTTTTACTAAAAGGATTGAGCC
GAATACAACAAAGATTCTATTGCATATATTTTGACTAAGTATATACTTACCTAGAT
ATACAAGATTTGAAATACAAAATCTAGcaagcttggtacc

SEQ. No. 3: cre coding region. sequence

gagctccATGgctagcTCC AATTTACTGA CCGTACACCA AAATTTGCCT
GCATTACCGG TCGATGCAAC GAGTGATGAG GTTCGCAAGA ACCTGATGGA
CATGTTCAGG GATCGCCAGG CGTTTTCTGA GCATACCTGG AAAATGCTTC
TGTCCGTTTG CCGGTCGTGG GCGGCATGGT GCAAGTTGAA TAACCGGAAA
TGGTTTCCCG CAGAACCTGA AGATGTTCGC GATTATCTTC TATATCTTCA
GGCGCGCGGT CTGGCAGTAA AAACTATCCA GCAACATTTG GGCCAGCTAA
ACATGCTTCA TCGTCGGTCC GGGCTGCCAC GACCAAGTGA CAGCAATGCT
GTTTCACTGG TTATGCGGCG GATCCGAAAA GAAAACGTTG ATGCCGGTGA

ACGTGCAAAA CAGGCTCTAG CGTTCGAACG CACTGATTTC GACCAGGTTC
GTTCACTCAT GGAAAATAGC GATCGCTGCC AGGATATACG TAATCTGGCA
TTTCTGGGGA TTGCTTATAA CACCCTGTTA CGTATAGCCG AAATTGCCAG
GATCAGGGTT AAAGATATCT CACGTACTGA CGGTGGGAGA ATGTTAATCC
ATATTGGCAG AACGAAAACG CTGGTTAGCA CCGCAGGTGT AGAGAAGGCA
CTTAGCCTGG GGGTAACTAA ACTGGTCGAG CGATGGATTT CCGTCTCTGG
TGTAGCTGAT GATCCGAATA ACTACCTGTT TTGCCGGGTC AGAAAAAATG
GTGTTGCCGC GCCATCTGCC ACCAGCCAGC TATCAACTCG CGCCCTGGAA
GGGATTTTTG AAGCAACTCA TCGATTGATT TACGGCGCTA AGGATGACTC
TGGTCAGAGA TACCTGGCCT GGTCTGGACA CAGTGCCCGT GTCGGAGCCG
CGCGAGATAT GGCCCGCGCT GGAGTTTCAA TACCGGAGAT CATGCAAGCT
GGTGGCTGGA CCAATGTAAA TATTGTCATG AACTATATCC GTAACCTGGA
TAGTGAAACA GGGGCAATGG TGCGCCTGCT cGAgGATGGC GATTAGtctaga

SEQ. No. 4: PrrnloxD. Sequence

gagctcGCTCCCCCGCCGTCGTTCAATGAGAATGGATAAGAGGCTCGTGGGATTGA
CGTGAGGGGGCAGGGATGGCTATATTTCTGGGAGCataacttcgtataatgtatgc
tatacgaagttatgaattc

SEQ. No. 5: TrbcL1oxD. sequence

tctagataacttcgtataatgtatgctatacgaagttatAGACATTAGCAGATAAA
TTAGCAGGAAATAAAGAAGGATAAGGAGAAAGAACTCAAGTAATTATCCTTCGTTC
TCTTAATTGAATTGCAATTAAACTCGGCCCAATCTTTTACTAAAAGGATTGAGCCG
AATACAACAAAGATTCTATTGCATATATTTTGACTAAGTATATACTTACCTAGATA
TACAAGATTTGAAATACAAAATCTAGcaagcttggtacc

SEQ. No. 6: Pea ssuTP5. sequence

ccggatccAA TTCAACCACA AGAACTAACA AAGTCAGAAA AATGGCTTCT
ATGATATCCT CTTCCGCTGT GACAACAGTC AGCCGTGCTT CTAGGGTGCA
ATCCGCGGCA GTGGCTCCAT TCGGCGGCCT GAAATCCATG ACTGGATTCC
CAGTGAAGAA GGTCAACACT GACATTACTT CCATTACAAG CAATGGTGGA
AGAGTAAAGT GCATGCAGGT GTGGCCTgcc atggctagc

SEQ. No. 7: Pea ssuTP22. sequence

ccggatcc AA TTCAACCACA AGAACTAACA AAGTCAGAAA AATGGCTTCT
ATGATATCCT CTTCCGCTGT GACAACAGTC AGCCGTGCTT CTAGGGTGCA
ATCCGCGGCA GTGGCTCCAT TCGGCGGCCT GAAATCCATG ACTGGATTCC
CAGTGAAGAA GGTCAACACT GACATTACTT CCATTACAAG CAATGGTGGA
AGAGTAAAGT GCATGCAGGT GTGGCCTCCA ATTGGAAAGA AGAAGTTTGA
GACTCTTTCC TATTTGCCAC CATTGACCat ggctagc

SEQ. No. 8: Pea ssuTP23. sequence

ccggatccAA TTCAACCACA AGAACTAACA AAGTCAGAAA AATGGCTTCT
ATGATATCCT CTTCCGCTGT GACAACAGTC AGCCGTGCTT CTAGGGTGCA
ATCCGCGGCA GTGGCTCCAT TCGGCGGCCT GAAATCCATG ACTGGATTCC
CAGTGAAGAA GGTCAACACT GACATTACTT CCATTACAAG CAATGGTGGA
AGAGTAAAGT GCATGCAGGT GTGGCCTCCA ATTGGAAAGA AGAAGTTTGA
GACTCTTTCC TATTTGCCAC CATTGACCAG AGATCAGTTG gctagcgg

SEQ. No. 9: P2 promoter sequence

gaattCATTT TCACGTGTGG AAGATATGAA TTTTTTTGAG AAACTAGATA
AGATTAATGA ATATCGGTGT TTTGGTTTTT TCTTGTGGCC GTCTTTGTTT
ATATTGAGAT TTTTCAAATC AGTGCGCAAG ACGTGACGTA AGTATCTGAG
CTAGTTTTTA TTTTTCTACT AATTTGGTCG TTTATTTCGG CGTGTAGGAC
ATGGCAACCG GGCCTGAATT TCGCGGGTAT TCTGTTTCTA TTCCAACTTT
TTCTTGATCC GCAGCCATTA ACGACTTTTG AATAGATACG CTGACACGCC
AAGCCTCGCT AGTCAAAAGT GTACCAAACA ACGCTTTACA GCAAGAACGG
AATGCGCGTG ACGCTCGCGG TGACGCCATT TCGCCTTTTC AGAAATGGAT
AAATAGCCTT GCTTCCTATT ATATCTTCCC AAATTACCAA TACATTACAC
TAGCATCTGA ATTTCATAAC CAATCTCGAT ACACCAAATC GATaggatcc
taccatgg

SEQ. No. 10: 35S promoter sequence

AAGCTTGCCA ACATGGTGGA GCACGACACT CTCGTCTACT CCAAGAATAT
CAAAGATACA GTCTCAGAAG ACCAAAGGGC TATTGAGACT TTTCAACAAA
GGGTAATATC GGGAAACCTC CTCGGATTCC ATTGCCCAGC TATCTGTCAC
TTCATCAAAA GGACAGTAGA AAAGGAAGGT GGCACCTACA AATGCCATCA
TTGCGATAAA GGAAAGGCTA TCGTTCAAGA TGCCTCTGCC GACAGTGGTC
CCAAAGATGG ACCCCCACCC ACGAGGAGCA TCGTGGAAAA AGAAGACGTT
CCAACCACGT CTTCAAAGCA AGTGGATTGA TGTGATAACA TGGTGGAGCA
CGACACTCTC GTCTACTCCA AGAATATCAA AGATACAGTC TCAGAAGACC
AAAGGGCTAT TGAGACTTTT CAACAAAGGG TAATATCGGG AAACCTCCTC
GGATTCCATT GCCCAGCTAT CTGTCACTTC ATCAAAAGGA CAGTAGAAAA
GGAAGGTGGC ACCTACAAAT GCCATCATTG CGATAAAGGA AAGGCTATCG
TTCAAGATGC CTCTGCCGAC AGTGGTCCCA AAGATGGACC CCCACCCACG
AGGAGCATCG TGGAAAAAGA AGACGTTCCA ACCACGTCTT CAAAGCAAGT
GGATTGATGT GATATCTCCA CTGACGTAAG GGATGACGCA CAATCCCACT
ATCCTTCGCA AGACCCTTCC TCTATATAAG GAAGTTCATT TCATTTGGAG
AGGACACGCT GAAATCACCA GTCTCTCTCT ACAAATCTAT CTCTCTCGAT
TCGCGAGCTC GGTACCCGGG gatcgatcc

SEQ. No. 11: KpnI-lox-BglII-lox-HindIII fragment

ggtaccATAACTTCGTATAATGTATGCTATACGAAGTTATagatctATAACTTCGT
ATAATGTATGCTATACGAAGTTATaagctt

Seq. ID No. 12. Translational coupling of *bar* and *aadA* according to scheme in Fig. 18. BglII-SpeI fragment.

GAGATCTGgg aggaataact tATGggggtc gacATAACTT CGTATAATGT
ATGCTATACG AAGTTATtaG AAGCGGTGAT CGCCGAAGTA TCGACTCAAC

TATCAGAGGT AGTTGGCGTC ATCGAGCGCC ATCTCGAACC GACGTTGCTG
GCCGTACATT TGTACGGCTC CGCAGTGGAT GGCGGCCTGA AGCCACACAG
TGATATTGAT TTGCTGGTTA CGGTGACCGT AAGGCTTGAT GAAACAACGC
GGCGAGCTTT GATCAACGAC CTTTTGGAAA CTTCGGCTTC CCCTGGAGAG
AGCGAGATTC TCCGCGCTGT AGAAGTCACC ATTGTTGTGC ACGACGACAT
CATTCCGTGG CGTTATCCAG CTAAGCGCGA ACTGCAATTT GGAGAATGGC
AGCGCAATGA CATTCTTGCA GGTATCTTCG AGCCAGCCAC GATCGACATT
GATCTGGCTA TCTTGCTGAC AAAAGCAAGA GAACATAGCG TTGCCTTGGT
AGGTCCAGCG GCGGAGGAAC TCTTTGATCC GGTTCCTGAA CAGGATCTAT
TTGAGGCGCT AAATGAAACC TTAACGCTAT GGAACTCGCC GCCCGACTGG
GCTGGCGATG AGCGAAATGT AGTGCTTACG TTGTCCCGCA TTTGGTACAG
CGCAGTAACC GGCAAAATCG CGCCGAAGGA TGTCGCTGCC GACTGGGCAA
TGGAGCGCCT GCCGGCCCAG TATCAGCCCG TCATACTTGA AGCTAGACAG
GCTTATCTTG GACAAGAAGA AGATCGCTTG GCCTCGCGCG CAGATCAGTT
GGAAGAATTT GTCCACTACG TGAAAGGCGA GATCACCAAG GTAGTCGGCA
AATAAATAAC TTCGTATAAT GTATGCTATA CGAAGTTATa ctagt

Seq. ID No. 13. CRE-induced expression of recombinant protein according to design in Fig. 19. SacI-NheI fragment.

gagctcGCTC CCCCGCCGTC GTTCAATGAG AATGGATAAG AGGCTCGTGG
GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAG AATTAACCGA
TCGACGTGCa AGCGGACATT TATTTTaAAT TCGATAATTT TTGCAAAAAC
ATTTCGACAT ATTTATTTAT TTTATTATTA TGgggATAAC TTCGTATAAT
GTATGCTATA CGAAGTTATt aGAAGCGGTG ATCGCCGAAG TATCGACTCA
ACTATCAGAG GTAGTTGGCG TCATCGAGCG CCATCTCGAA CCGACGTTGC
TGGCCGTACA TTTGTACGGC TCCGCAGTGG ATGGCGGCCT GAAGCCACAC
AGTGATATTG ATTTGCTGGT TACGGTGACC GTAAGGCTTG ATGAAACAAC
GCGGCGAGCT TTGATCAACG ACCTTTTGGA AACTTCGGCT TCCCCTGGAG
AGAGCGAGAT TCTCCGCGCT GTAGAAGTCA CCATTGTTGT GCACGACGAC
ATCATTCCGT GGCGTTATCC AGCTAAGCGC GAACTGCAAT TTGGAGAATG
GCAGCGCAAT GACATTCTTG CAGGTATCTT CGAGCCAGCC ACGATCGACA
TTGATCTGGC TATCTTGCTG ACAAAAGCAA GAGAACATAG CGTTGCCTTG
GTAGGTCCAG CGGCGGAGGA ACTCTTTGAT CCGGTTCCTG AACAGGATCT
ATTTGAGGCG CTAAATGAAA CCTTAACGCT ATGGAACTCG CCGCCCGACT
GGGCTGGCGA TGAGCGAAAT GTAGTGCTTA CGTTGTCCCG CATTTGGTAC
AGCGCAGTAA CCGGCAAAAT CGCGCCGAAG GATGTCGCTG CCGACTGGGC
AATGGAGCGC CTGCCGGCCC AGTATCAGCC CGTCATACTT GAAGCTAGAC
AGGCTTATCT TGGACAAGAA GAAGATCGCT TGGCCTCGCG CGCAGATCAG
TTGGAAGAAT TTGTCCACTA CGTGAAAGGC GAGATCACCA AGGTAGTCGG
CAAATAAATA ACTTCGTATA ATGTATGCTA TACGAAGTTA Ttagctagc

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While certain of the preferred embodiments of the present invention have been described and specifically exemplified above, it is not intended that the invention be limited to such embodiments. Various modifications may be made thereto without departing from the scope and spirit of the present invention, as set forth in the following claims.